AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings of claims in the application.

Listing of claims

1. (Currently amended) A method ~~for~~ of identifying ~~an individual who has~~ a human having an altered risk for developing Alzheimer's disease, comprising detecting the presence of a single nucleotide polymorphism (SNP) at position 101 of SEQ ID NO: 7368 or its complement thereof ~~in any one of the nucleotide sequences of SEQ ID NOS:1-433 and 867-54,769~~ in said ~~individual's~~ human's nucleic acids, wherein the presence of the SNP is ~~correlated with~~ indicative of an altered risk for Alzheimer's disease in said ~~individual~~ human.

2. - 35. (Canceled)

36. (New) The method of claim 1 in which said human has Alzheimer's disease.

37. (New) The method of claim 1 in which SEQ ID NO: 7368 is contained within the genomic sequence as represented by SEQ ID NO: 6756.

38. (New) The method of claim 1 in which the SNP to be detected is located at position 41788 of SEQ ID NO: 6756.

39. (New) The method of claim 1 in which said human's nucleic acids are extracted from a biological sample therefrom.

40. (New) The method of claim 39 in which said biological sample is blood.

41. (New) The method of claim 1 in which said human's nucleic acids are amplified before the detection is carried out.

42. (New) The method of claim 1 in which detection is carried out by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 55277, SEQ ID NO: 55278, and SEQ ID NO: 55279.

43. (New) The method of claim 1 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

44. (New) A method of identifying a human having an increased risk for developing Alzheimer's disease, comprising detecting the presence of a single nucleotide polymorphism (SNP) at position 101 of SEQ ID NO: 7368 or its complement thereof in said human's nucleic acids, wherein the presence of C at position 101 of SEQ ID NO: 7368 is indicative of an increased risk for myocardial infarction in said human.

45. (New) The method of claim 44 in which said human has Alzheimer's disease.

46. (New) The method of claim 44 in which SEQ ID NO: 7368 is contained within the genomic sequence as represented by SEQ ID NO: 6756.

47. (New) The method of claim 44 in which the SNP to be detected is located at position 41788 of SEQ ID NO: 6756.

48. (New) The method of claim 44 in which said human's nucleic acids are extracted from a biological sample therefrom.

49. (New) The method of claim 48 in which said biological sample is blood.

50. (New) The method of claim 44 in which said human's nucleic acids are amplified before the detection is carried out.

51. (New) The method of claim 44 in which detection is carried out by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 55277, SEQ ID NO: 55278, and SEQ ID NO: 55279.

52. (New) The method of claim 44 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

53. (New) A method of identifying a human having a decreased risk for developing Alzheimer's disease, comprising detecting the presence of a single nucleotide polymorphism (SNP) at position 101 of SEQ ID NO: 7368 or its complement thereof in said human's nucleic acids, wherein the presence of T at position 101 of SEQ ID NO: 7368 is indicative of a decreased risk for myocardial infarction in said human.

54. (New) The method of claim 44 in which said human has Alzheimer's disease.

55. (New) The method of claim 53 in which SEQ ID NO: 7368 is contained within the genomic sequence as represented by SEQ ID NO: 6756.

56. (New) The method of claim 53 in which the SNP to be detected is located at position 41788 of SEQ ID NO: 6756.

57. (New) The method of claim 53 in which said human's nucleic acids are extracted from a biological sample therefrom.

58. (New) The method of claim 57 in which said biological sample is blood.

59. (New) The method of claim 53 in which said human's nucleic acids are amplified before the detection is carried out.

60. (New) The method of claim 53 in which detection is carried out by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 55277, SEQ ID NO: 55278, and SEQ ID NO: 55279.

61. (New) The method of claim 53 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

62. (New) A method of determining a human's risk for developing Alzheimer's disease, comprising detecting a single nucleotide polymorphism (SNP) at position 101 of SEQ ID NO: 7368 or its complement thereof in said human's nucleic acids, wherein the presence of C at position 101 of SEQ ID NO: 7368 is indicative of an increased risk for myocardial infarction in said human, or the presence of T at position 101 of SEQ ID NO: 7368 is indicative of a decreased risk for developing myocardial infarction in said human.

63. (New) The method of claim 62 in which said human has Alzheimer's disease.

64. (New) The method of claim 62 in which SEQ ID NO: 7368 is contained within the genomic sequence of LRP2 gene as represented by SEQ ID NO: 6756.

65. (New) The method of claim 62 in which the SNP to be detected is located at position 41788 of SEQ ID NO: 6756.

66. (New) The method of claim 62 in which said human's nucleic acids are extracted from a biological sample therefrom.

67. (New) The method of claim 66 in which said biological sample is blood.

68. (New) The method of claim 62 in which said human's nucleic acids are amplified before the detection is carried out.

69. (New) The method of claim 62 in which detection is carried out by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 55277, SEQ ID NO: 55278, and SEQ ID NO: 55279.

70. (New) The method of claim 62 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.